RAW SEQUENCE LISTING

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Application Serial Number: 10/527,788
Source: PCT
Date Processed by STIC: 03/06/2006

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RAW SEQUENCE LISTING DATE: 03/06/2006
PATENT APPLICATION: **US/10/527,788** TIME: 15:55:24

Input Set : **A:\63047451.APP**
Output Set: **N:\CRF4\03062006\J527788.raw**

<110> APPLICANT: WOLF, SABINE
JAGER, MARTINA
BANGSOW, THORSTEN
BANGSOW, CARMEN
JORDAN, DOMINIK
PELZER, BERNHARD
OPPOLZER, THOMAS
<120> TITLE OF INVENTION: METHOD FOR IDENTIFYING BBB-SPECIFIC PROTEINS AND FRAGMENTS THEREOF
<130> FILE REFERENCE: 63047(45107)
<140> CURRENT APPLICATION NUMBER: 10/527,788
<141> CURRENT FILING DATE: 2005-03-11
<150> PRIOR APPLICATION NUMBER: PCT/EP03/09968
<151> PRIOR FILING DATE: 2003-03-08
<150> PRIOR APPLICATION NUMBER: DE 102 42 016.5
<151> PRIOR FILING DATE: 2002-09-11
<160> NUMBER OF SEQ ID NOS: 70
<170> SOFTWARE: PatentIn Ver. 3.3
<210> SEQ ID NO: 1
<211> LENGTH: 323
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic clone S129 from BMEC from swine brain
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tggtgaaaat cgccttcaat acacccgcag cggtgcaaaa agaggaggcg cagcaagacg 120
tggaggccct cgtaagccat acggtccgtg ctcagatcct gactggcaag gaactccaag 180
ttgccactaa ggaaaaagag ggcttctctg ggagatgcat gcttactctc gtaggccttt 240
ccttcatctt ggcaggactt attgttggtg gagcctgcat ttacaagtac ttcatgccca 300
agagtaccat actaccatgg aga 323
<210> SEQ ID NO: 2
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
<400> SEQUENCE: 2
acctccattg ttatgcctcc ta 22
<210> SEQ ID NO: 3
<211> LENGTH: 22

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62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
67       primer
69 <400> SEQUENCE: 3
70 gttgcctctc actcttgaca ga                                              22
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 1598
75 <212> TYPE: DNA
76 <213> ORGANISM: Sus sp.
78 <220> FEATURE:
79 <221> NAME/KEY: CDS
80 <222> LOCATION: (119)..(910)
82 <220> FEATURE:
83 <221> NAME/KEY: modified_base
84 <222> LOCATION: (1168)
85 <223> OTHER INFORMATION: a, c, g, t, unknown, or other
87 <400> SEQUENCE: 4
88 gcggccgcta gcataaagaa ggtgattcta agcctagcgc tatcttctcc tagtccagcc 60
90 tgcagccgag gacaacactg attcgagccg tgacctaccg gccgcgggaa ttcgattt   118
92 atg gtg aaa atc gcc ttc aat aca ccc gca gcg gtg caa aaa gag gag   166
93 Met Val Lys Ile Ala Phe Asn Thr Pro Ala Ala Val Gln Lys Glu Glu
94   1               5                  10                  15
96 gcg cag caa gac gtg gag gcc ctc gta agc cat acg gtc cgt gct cag   214
97 Ala Gln Gln Asp Val Glu Ala Leu Val Ser His Thr Val Arg Ala Gln
98              20                  25                  30
100 atc ctg act ggc aag gaa ctc caa gtt gcc act aag gaa aaa gag ggc   262
101 Ile Leu Thr Gly Lys Glu Leu Gln Val Ala Thr Lys Glu Lys Glu Gly
102          35                  40                  45
104 ttc tct ggg aga tgc atg ctt act ctc gta ggc ctt tcc ttc atc ttg   310
105 Phe Ser Gly Arg Cys Met Leu Thr Leu Val Gly Leu Ser Phe Ile Leu
106      50                  55                  60
108 gca gga ctt att gtt ggt gga gcc tgc att tac aag tac ttc atg ccc   358
109 Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
110  65                  70                  75                  80
112 aag agt acc atc tac cat gga gag atg tgc ttc ttt gat tct gcg gac   406
113 Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Ala Asp
114                  85                  90                  95
116 cct gca aat ttc ctc caa gga gga gag ccc tac ttc ctg cct gtg atg   454
117 Pro Ala Asn Phe Leu Gln Gly Gly Glu Pro Tyr Phe Leu Pro Val Met
118              100                 105                 110
120 gaa gag gct gat att cgt gaa gat gac aac att gca atc att gat gtg   502
121 Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val
122          115                 120                 125
124 cct gtc ccc agt ttc tct gat agt gac cct gca gca att att cat gac   550
125 Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp
126      130                 135                 140
128 ttt gaa aag ggc atg act gct tac ctg gac ttg ctg ctg ggg aac tgc   598
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129 Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys
130 145                 150                 155                 160
132 tat ctg atg ccc ctc aat acc tcc att gtt atg cct cct aag tat ctc   646
133 Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Tyr Leu
134                 165                 170                 175
136 gtg gag ctc ttt ggc aaa ctg gca cgt ggc aaa tac ctc cct cac gct   694
137 Val Glu Leu Phe Gly Lys Leu Ala Arg Gly Lys Tyr Leu Pro His Ala
138             180                 185                 190
140 tat gtg gtt cat gaa gac ctg gtt gct gtg gaa gag att cat gat gtt   742
141 Tyr Val Val His Glu Asp Leu Val Ala Val Glu Glu Ile His Asp Val
142         195                 200                 205
144 agt aac ctt ggc atc ttt att tac caa ctt tgc aac aac cgc aag tct   790
145 Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser
146     210                 215                 220
148 ttc cgc ctt cgt aga aga gac ctc ttg ctg ggt ttc aac aaa cgt gcc   838
149 Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
150 225                 230                 235                 240
152 att gat aag tgc tgg aag att aga cac ttc ccc aat gaa ttt att gtt   886
153 Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val
154                 245                 250                 255
156 gag acc aag atc tgt caa gag tga gaggcaacag aaaaagagtg tacttagtaa  940
157 Glu Thr Lys Ile Cys Gln Glu
158             260
160 taggaagtca aagatttaca atatgacttc aatattaaag tgtgtaggac attcaagata 1000
162 tttactcatg catttcctct attgcttata cttaaaaaaa agaaagaaaa taaaaactac 1060
164 taaccattgc aaaaaaaaaa aaaaaaagta ctagtcgacg cgtggccaga aactgaaatg 1120
W--> 166 aaatgatttt tatgtttttc cttttgaatt tatagggttt atgttttntt gaatgcaatg 1180
168 tgaaggtgtt ggctaacatc ctgacaatga attccatccc ttgtgtatat gtgtgtcttt 1240
170 aaaagtaaaa tyttcartca tatggtaaaa catgttttaa atttaaaata tttaaaattg 1300
172 ttttcaacct ttttgtgtag cgcttgtcaa atatcttaac attgtcttgt tttgttttca 1360
174 ttgtgtgcaa ctttcctgaa tttagaaatt aaatttttgc atttatgtta ggtgttctgt 1420
176 aatagatatg acttatatgt gaaaaacttt cataaagaag tcattttcac taatrcagtg 1480
178 actctcactg gtaactgtat tgtgaaatgc acaaaactgt tttagtgctg aatgctataa 1540
180 ggaatttagg ttgtatgaat tctacaatcc tataataaat tttaccatat tcaaaaaa   1598
183 <210> SEQ ID NO: 5
184 <211> LENGTH: 263
185 <212> TYPE: PRT
186 <213> ORGANISM: Sus sp.
188 <400> SEQUENCE: 5
189 Met Val Lys Ile Ala Phe Asn Thr Pro Ala Ala Val Gln Lys Glu Glu
190   1               5                  10                  15
192 Ala Gln Gln Asp Val Glu Ala Leu Val Ser His Thr Val Arg Ala Gln
193              20                  25                  30
195 Ile Leu Thr Gly Lys Glu Leu Gln Val Ala Thr Lys Glu Lys Glu Gly
196          35                  40                  45
198 Phe Ser Gly Arg Cys Met Leu Thr Leu Val Gly Leu Ser Phe Ile Leu
199      50                  55                  60
201 Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
202  65                  70                  75                  80
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```
204 Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Ala Asp
205                  85                  90                  95
207 Pro Ala Asn Phe Leu Gln Gly Gly Glu Pro Tyr Phe Leu Pro Val Met
208             100                 105                 110
210 Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val
211         115                 120                 125
213 Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp
214     130                 135                 140
216 Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys
217 145                 150                 155                 160
219 Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Tyr Leu
220                 165                 170                 175
222 Val Glu Leu Phe Gly Lys Leu Ala Arg Gly Lys Tyr Leu Pro His Ala
223             180                 185                 190
225 Tyr Val Val His Glu Asp Leu Val Ala Val Glu Glu Ile His Asp Val
226         195                 200                 205
228 Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser
229     210                 215                 220
231 Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
232 225                 230                 235                 240
234 Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val
235                 245                 250                 255
237 Glu Thr Lys Ile Cys Gln Glu
238             260
242 <210> SEQ ID NO: 6
243 <211> LENGTH: 814
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
249       clone S231 from BMEC from swine brain
251 <220> FEATURE:
252 <221> NAME/KEY: modified_base
253 <222> LOCATION: (712)
254 <223> OTHER INFORMATION: a, c, g, t, unknown, or other
256 <400> SEQUENCE: 6
257 acatttcttt aggttcattc tggttaaggg gatgttcgag ggtgggccac caaattgtct 60
258 gggctgggga taaagcagtt ggcaagcaaa aactatggga tgatgaactt ttcaatwatg 120
259 atttaatgat cacatgagta tagaaagctg ttttgagtgc tgaaacagac ttacctatca 180
260 gatatatcca aaagagattc tatgttaaaa agtcagacta tgactggagt gaaccatgta 240
261 ttcccttgtc ttttactttg tttctgtgac atttatgttt catgtaactt gcattatggt 300
262 tgggtgggtt gtcctagtac tgtattttgg cttcttcttt aataggattg atatttcata 360
263 tabtataatt gtgaatattt tgakacraat gtttataact ctaggcatat aaaaacagat 420
264 tctgattccc ttcactgtgt gaatgttttc tgttgaaaaa atggaggata aatatggata 480
265 ctaatgacac tcattcctaa ttaagttttc aatcagtttg atttggataa cttgcattta 540
266 tccgagatat tgagctactt tctgataatg catcaagcat ttctaccata actctttcac 600
267 gcaactgaat gttgttaagt atagttttat cttgctttaa ttaaacttct taagcaaaaa 660
W--> 268 aaaagaaact tcataagcta atacattaga gaaaggttat gatcttgaat cnagaatggc 720
269 ttatggcatt aaggaatgag atacttgtaa attttctttg aaacagccaa ctcctctgtt 780
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```
270 gtgtcttcac aattcaaaag atatgcctca ctgt                                814
273 <210> SEQ ID NO: 7
274 <211> LENGTH: 22
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
280       primer
282 <400> SEQUENCE: 7
283 ccataactct ttcacgcaac tg                                              22
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 22
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
293       primer
295 <400> SEQUENCE: 8
296 acaacagagg agttggctgt tt                                              22
299 <210> SEQ ID NO: 9
300 <211> LENGTH: 22
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
306       primer
308 <400> SEQUENCE: 9
309 ggtattgctg gctggtatct tt                                              22
312 <210> SEQ ID NO: 10
313 <211> LENGTH: 22
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
319       primer
321 <400> SEQUENCE: 10
322 atgtaggaat agccgtggtg at                                              22
325 <210> SEQ ID NO: 11
326 <211> LENGTH: 22
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
332       primer
334 <400> SEQUENCE: 11
335 ggtctttgtg ttccagctct tc                                              22
338 <210> SEQ ID NO: 12
339 <211> LENGTH: 23
340 <212> TYPE: DNA
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/06/2006
PATENT APPLICATION: **US/10/527,788** TIME: 15:55:25

Input Set : **A:\63047451.APP**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 1168
Seq#:6; N Pos. 712
Seq#:36; N Pos. 1443,1444,1445
Seq#:52; Xaa Pos. 61
Seq#:53; Xaa Pos. 61

VERIFICATION SUMMARY DATE: 03/06/2006
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L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1120
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:660
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:1440
L:1514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:671
L:1634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:48